

# FIG. 1

(SEQ ID NO: 1)

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gcgccgcgctc ccgcaggccg tgatgccgcc cgcgcgaggg tggcccggac cgcaagtgcc 60
caagagagct ctaatggtac caagtgcacag gttggcttta ctgtgactcg gggacgccag 120
agctcctgag aag atg tca gca ata cag gcc gcc tgg cca tcc ggt aca 169
      Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr
          1             5             10

gaa tgt att gcc aag tac aac ttc cac ggc act gcc gag cag gac ctg 217
Glu Cys Ile Ala Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu
      15             20             25

ccc ttc tgc aaa gga gac gtg ctc acc att gtg gcc gtc acc aag gac 265
Pro Phe Cys Lys Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp
      30             35             40

ccc aac tgg tac aaa gcc aaa aac aag gtg ggc cgt gag ggc atc atc 313
Pro Asn Trp Tyr Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile 60
      45             50             55

cca gcc aac tac gtc cag aag cgg gag ggc gtg aag gcg ggt acc aaa 361
Pro Ala Asn Tyr Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys
      65             70             75

ctc agc ctc atg cct tgg ttc cac ggc aag atc aca cgg gag cag gct 409
Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala
      80             85             90

gag cgg ctt ctg tac ccg ccg gag aca ggc ctg ttc ctg gtg cgg gag 457
Glu Arg Leu Leu Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu
      95             100            105

agc acc aac tac ccc gga gac tac acg ctg tgc gtg agc tgc gac ggc 505
Ser Thr Asn Tyr Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly
      110            115            120

aag gtg gag cac tac cgc atc atg tac cat gcc agc aag ctc agc atc 553
Lys Val Glu His Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile
      125            130            135

gac gag gag gtg tac ttt gag aac ctc atg cag ctg gtg gag cac tac 601
Asp Glu Glu Val Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr
      145            150            155

acc tca gac gca gat gga ctc tgt acg cgc ctc att aaa cca aag gtc 649
Thr Ser Asp Ala Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val
      160            165            170

atg gag ggc aca gtg gcg gcc cag gat gag ttc tac cgc agc ggc tgg 697
Met Glu Gly Thr Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp
      175            180            185

gcc ctg aac atg aag gag ctg aag ctg ctg cag acc atc ggg aag ggg 745
Ala Leu Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly
      190            195            200

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## FIG. 1 cont.

gag ttc gga gac gtg atg ctg ggc gat tac cga ggg aac aaa gtc gcc	793
Glu Phe Gly Asp Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala	
205 210 215 220	
gtc aag tgc att aag aac gac gcc act gcc cag gcc ttc ctg gct gaa	841
Val Lys Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu	
225 230 235	
gcc tca gtc atg acg caa ctg cgg cat agc aac ctg gtg cag ctc ctg	889
Ala Ser Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu	
240 245 250	
ggc gtg atc gtg gag gag aag ggc ggg ctc tac atc gtc act gag tac	937
Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr	
255 260 265	
atg gcc aag ggg agc ctt gtg gac tac ctg cgg tct agg ggt cgg tca	985
Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser	
270 275 280	
gtg ctg ggc gga gac tgt ctc ctc aag ttc tcg cta gat gtc tgc gag	1033
Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu	
285 290 295 300	
gcc atg gaa tac ctg gag ggc aac aat ttc gtg cat cga gac ctg gct	1081
Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala	
305 310 315	
gcc cgc aat gtg ctg gtg tct gag gac aac gtg gcc aag gtc agc gac	1129
Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp	
320 325 330	
ttt ggt ctc acc aag gag gcg tcc agc acc cag gac acg ggc aag ctg	1177
Phe Gly Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu	
335 340 345	
cca gtc aag tgg aca gcc cct gag gcc ctg aga gag aag aaa ttc tcc	1225
Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser	
350 355 360	
act aag tct gac gtg tgg agt ttc gga atc ctt ctc tgg gaa atc tac	1273
Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr	
365 370 375 380	
tcc ttt ggg cga gtg cct tat cca aga att ccc ctg aag gac gtc gtc	1321
Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val	
385 390 395	
cct cgg gtg gag aag ggc tac aag atg gat gcc ccc gac ggc tgc ccg	1369
Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro	
400 405 410	
ccc gca gtc tat gaa gtc atg aag aac tgc tgg cac ctg gac gcc gcc	1417
Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala	
415 420 425	

## FIG. 1 cont.

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atg cgg ccc tcc ttc cta cag ctc cga gag cag ctt gag cac atc aaa 1465
Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys
    430                435                440

acc cac gag ctg cac ctg tgaaggctgg cctccgctg ggtcatgggc 1513
Thr His Glu Leu His Leu
    445                450

ctgtggggac tgaacctgga agatcatgga cctgggtgcc ctgctcactg ggcccagagcc 1573
tgaactgagc cccagcgggc tggcgggcct ttttctgcg tcccagcctg caccctccg 1633
gccccgtctc tcttggaacc acctgtgggg cctggggagc ccactgaggg gccagggagg 1693
aaggaggcca cggagcggga ggcagcgccc caccacgtcg ggcttcctg gcctcccgc 1753
actcgccctc ttagagtttt attcctttcc ttttttgaga tttttttcc gtgtgtttat 1813
tttttattat ttttcaagat aaggagaaag aaagtacca gcaaattggc attttacaag 1873
aagtacgaat cttatcttct ctgtcctgcc cgtgaggggtg ggggggaccg ggcccctctc 1933
tagggacccc tcgccccagc ctcatctccc attctgtgtc ccatgtcccg tgtctcctcg 1993
gtcgccccgt gtttgcgctt gaccatgttg cactgtttgc atgcgcccga ggcagacgtc 2053
tgtcaggggc ttggatttcg tgtgccgtg ccaccgccc acccgcttg tgagatggaa 2113
ttgtaataaa ccacgccatg aggacaccgc cgccgcctc ggcgcttcct ccaccgaaaa 2173
aaaaaaaaaa aaaa 2187

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## FIG. 2

[illegible]

# FIG. 3

(SEQ ID NO: 3)

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gcgagaccaa ggcacacggg tctgaccctt gggccggccc ggagcaagtg acacggaccg 60
gtcgcctatc ctgaccacag caaagcggcc cggagcccgc ggaggggacc tgacgggggc 120
gtaggcgccg gaaggctggg ggccccggag ccgggcccgc gtggcccagag ttccggtgag 180
cggacggcgg cgcgcgcaga tttgata atg ggc tgc att aaa agt aaa gaa aac 234
                               1       5
                               Met Gly Cys Ile Lys Ser Lys Glu Asn
aaa agt cca gcc att aaa tac aga cct gaa aat act cca gag cct gtc 282
Lys Ser Pro Ala Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val
10              15              20              25

agt aca agt gtg agc cat tat gga gca gaa ccc act aca gtg tca cca 330
Ser Thr Ser Val Ser His Tyr Gly Ala Glu Pro Thr Thr Val Ser Pro
              30              35              40

tgt ccg tca tct tca gca aag gga aca gca gtt aat ttc agc agt ctt 378
Cys Pro Ser Ser Ser Ala Lys Gly Thr Ala Val Asn Phe Ser Ser Leu
              45              50              55

tcc atg aca cca ttt gga gga tcc tca ggg gta acg cct ttt gga ggt 426
Ser Met Thr Pro Phe Gly Gly Ser Ser Gly Val Thr Pro Phe Gly Gly
              60              65              70

gca tct tcc tca ttt tca gtg gtg cca agt tca tat cct gct ggt tta 474
Ala Ser Ser Ser Phe Ser Val Val Pro Ser Ser Tyr Pro Ala Gly Leu
              75              80              85

aca ggt ggt gtt act ata ttt gtg gcc tta tat gat tat gaa gct aga 522
Thr Gly Gly Val Thr Ile Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
90              95              100              105

act aca gaa gac ctt tca ttt aag aag ggt gaa aga ttt caa ata att 570
Thr Thr Glu Asp Leu Ser Phe Lys Lys Gly Glu Arg Phe Gln Ile Ile
              110              115              120

aac aat acg gaa gga gat tgg tgg gaa gca aga tca atc gct aca gga 618
Asn Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Ile Ala Thr Gly
              125              130              135

aag aat ggt tat atc ccg agc aat tat gta gcg cct gca gat tcc att 666
Lys Asn Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ala Asp Ser Ile
              140              145              150

cag gca gaa gaa tgg tat ttt ggc aaa atg ggg aga aaa gat gct gaa 714
Gln Ala Glu Glu Trp Tyr Phe Gly Lys Met Gly Arg Lys Asp Ala Glu
155              160              165

aga tta ctt ttg aat cct gga aat caa cga ggt att ttc tta gta aga 762
Arg Leu Leu Leu Asn Pro Gly Asn Gln Arg Gly Ile Phe Leu Val Arg
170              175              180              185

gag agt gaa aca act aaa ggt gct tat tcc ctt tct att cgt gat tgg 810
Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
              190              195              200

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### FIG. 3 cont.

gat gag ata agg ggt gac aat gtg aaa cac tac aaa att agg aaa ctt	858
Asp Glu Ile Arg Gly Asp Asn Val Lys His Tyr Lys Ile Arg Lys Leu	
205 210 215	
gac aat ggt gga tac tat atc aca acc aga gca caa ttt gat act ctg	906
Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Leu	
220 225 230	
cag aaa ttg gtg aaa cac tac aca gaa cat gct gat ggt tta tgc cac	954
Gln Lys Leu Val Lys His Tyr Thr Glu His Ala Asp Gly Leu Cys His	
235 240 245	
aag ttg aca act gtg tgt cca act gtg aaa cct cag act caa ggt cta	1002
Lys Leu Thr Thr Val Cys Pro Thr Val Lys Pro Gln Thr Gln Gly Leu	
250 255 260 265	
gca aaa gat gct tgg gaa atc cct cga gaa tct ttg cga cta gag gtt	1050
Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val	
270 275 280	
aaa cta gga caa gga tgt ttc ggc gaa gtg tgg atg gga aca tgg aat	1098
Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn	
285 290 295	
gga acc acg aaa gta gca atc aaa aca cta aaa cca ggt aca atg atg	1146
Gly Thr Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Met	
300 305 310	
cca gaa gct ttc ctt caa gaa gct cag ata atg aaa aaa tta aga cat	1194
Pro Glu Ala Phe Leu Gln Glu Ala Gln Ile Met Lys Lys Leu Arg His	
315 320 325	
gat aaa ctt gtt cca cta tat gct gtt gtt tct gaa gaa cca att tac	1242
Asp Lys Leu Val Pro Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr	
330 335 340 345	
att gtc act gaa ttt atg tca aaa gga agc tta tta gat ttc ctt aag	1290
Ile Val Thr Glu Phe Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys	
350 355 360	
gaa gga gat gga aag tat ttg aag ctt cca cag ctg gtt gat atg gct	1338
Glu Gly Asp Gly Lys Tyr Leu Lys Leu Pro Gln Leu Val Asp Met Ala	
365 370 375	
gct cag att gct gat ggt atg gca tat att gaa aga atg aac tat att	1386
Ala Gln Ile Ala Asp Gly Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile	
380 385 390	
cac cga gat ctt cgg gct gct aat att ctt gta gga gaa aat ctt gtg	1434
His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val	
395 400 405	
tgc aaa ata gca gac ttt ggt tta gca agg tta att gaa gac aat gaa	1482
Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu	
410 415 420 425	
tac aca gca aga caa ggt gca aaa ttt cca atc aaa tgg aca gct cct	1530
Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro	
430 435 440	

## FIG. 3 cont.

gaa gct gca ctg tat ggt cgg ttt aca ata aag tct gat gtc tgg tca	1578
Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser	
445 450 455	
ttt gga att ctg caa aca gaa cta gta aca aag ggc cga gtg cca tat	1626
Phe Gly Ile Leu Gln Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr	
460 465 470	
cca ggt atg gtg aac cgt gaa gta cta gaa caa gtg gag cga gga tac	1674
Pro Gly Met Val Asn Arg Glu Val Leu Glu Gln Val Glu Arg Gly Tyr	
475 480 485	
agg atg ccg tgc cct cag ggc tgt cca gaa tcc ctc cat gaa ttg atg	1722
Arg Met Pro Cys Pro Gln Gly Cys Pro Glu Ser Leu His Glu Leu Met	
490 495 500 505	
aat ctg tgt tgg aag aag gac cct gat gaa aga cca aca ttt gaa tat	1770
Asn Leu Cys Trp Lys Lys Asp Pro Asp Glu Arg Pro Thr Phe Glu Tyr	
510 515 520	
att cag tcc ttc ttg gaa gac tac ttc act gct aca gag cca cag tac	1818
Ile Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro Gln Tyr	
525 530 535	
cag cca gga gaa aat tta taattcaagt agcctatattt atatgcacaa	1866
Gln Pro Gly Glu Asn Leu	
540	
atctgccaaa atataaagaa cttgtgtaga ttttctacag gaatcaaaag aagaaaatct	1926
tctttactct gcatgttttt aatggtaaac tggaatccca gatatgggtg cacaaaacca	1986
cttttttttc cccaagtatt aaactctaata gtaccaatga tgaatttatc agcgtatttc	2046
agggtccaaa caaaatagag ctaagatact gatgacagtg tgggtgacag catggtaatg	2106
aaggacagtg aggctcctgc ttatttataa atcatttcct ttcttttttt ccccaaagtc	2166
agaattgctc aaagaaaatt atttattggt acagataaaa cttgagagat aaaaagctat	2226
accataataa aatctaaaat taaggaatat catgggacca aataattcca ttccagtttt	2286
ttaaagtttc ttgcatttat tattctcaaa agttttttct aagttaaaca gtcagtatgc	2346
aatcttaata tatgctttct tttgcatgga catgggccag gtttttcaaa aggaatataa	2406
acaggatctc aaacttgatt aaatgttaga ccacagaagt ggaatttgaa agtataatgc	2466
agtacattaa tttcatgtt catggaactg aaagaataag aactttttca cttcagtcct	2526
tttctgaaga gtttgactta gaataatgaa ggtaactaga aagtgagtta atcttgatg	2586
aggttgcatt gattttttta ggcaatatat aattgaaact actgtccaat caaaggggaa	2646
atgttttgat ctttagatag catgcaaagt aagaccagc attttaaaag ccctttttta	2706
aaaactagac ttcgtactgt gagtattgct tatatgtcct tatggggatg ggtgccacaa	2766
atagaaaata tgaccagatc agggacttga atgcactttt gtcacatggtg aatatagatg	2826

## FIG. 3 cont.

aacagagagg aaaatgtatt taaaagaaat acgagaaaag aaaatgtgaa agttttacaa 2886  
gtagagggga tggaaggtaa tgtttaaatgt tgatgtcatg gagtgacaga atggctttgc 2946  
tggcactcag agctcctcac ttagctatat tctgagactt tgaagagtta taaagtataa 3006  
ctataaaact aatttttctt acacactaaa tgggtatttg ttcaaaataa tgaagttatg 3066  
gcttcacatt cattgcagtg ggatatgggt tttatgtaaa acatttttag aactccagtt 3126  
ttcaaatcat gtttgaatct acattcactt ttttttgttt tcttttttga gacggagtct 3186  
cgctctgccg ccagggctgg agtgcagtg cgcatctcg gctcactgca agctctgcct 3246  
cccaggttca caccattctc ctgcctcagc ctcccagta gctgggacta caggtgccca 3306  
ccaccacgcc tggctagttt tttgtatttt tagtagagac gcagtttcac cgtgttagcc 3366  
aggatggtct cgatctcctg accttgtgat ctgccgcct cggcctcca aagtgtggg 3426  
attacaggtg tgagccaccg cgccagcct acattcactt ctaaagtcta tgtaatggtg 3486  
gtcatttttt cccttttaga atacattaaa tgggtgattt ggggaggaaa acttattctg 3546  
aatattaacg gtggtgaaaa ggggacagtt tttaccctaa agtgcaaaag tgaaacatac 3606  
aaaataagac taatttttta gagtaactca gtaatttcaa aatacagatt tgaatagcag 3666  
cattagtggg ttgagtgtct agcaaaggaa aaattgatga ataaaaatgaa ggtctggtgt 3726  
atatgtttta aaatactctc atatagtcac actttaaatt aagccttata ttagggccct 3786  
ctattttcag gatataattc ttaactatca ttatttacct gattttaatc atcagattcg 3846  
aaattctgtg ccatggcgta tatgttcaaa ttcaaaccat ttttaaaatg tgaagatgga 3906  
cttcatgcaa gttggcagtg gttctggtac taaaaattgt ggttgttttt tctgtttacg 3966  
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tatttctct tatcaacaac ttgtgacatg agatttttta agggctttat gtgaactatg 4086  
atattgtaat ttttctaagc atattcaaaa gggtgacaaa attacgttta tgtactaaat 4146  
ctaatacagga aagtaaggca ggaaaagttg atggtattca ttaggtttta actgaatgga 4206  
gcagttcctt atataataac aattgtatag tagggataaa aactaaciaa tgtgtattca 4266  
ttttaaatg tttctgtattt ttaaattgcc aagaaaaaca actttgtaaa tttggagata 4326  
ttttccaaca gcttttcgtc ttcagtgtct taatgtggaa gttaaccctt accaaaaaag 4386  
gaagttggca aaaacagcct tctagcacac ttttttaaat gaataatggt agcctaaact 4446  
taatattttt ataaagtatt gtaatattgt tttgtggata attgaaataa aaagttctca 4506  
ttgaatgcac c 4517



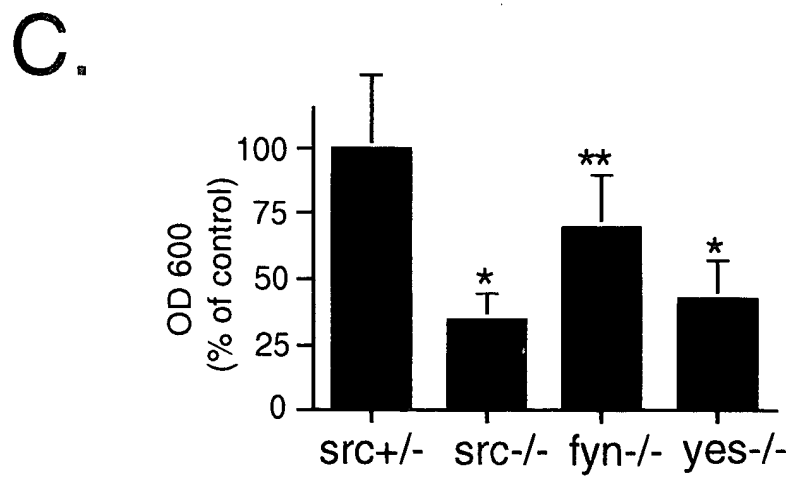
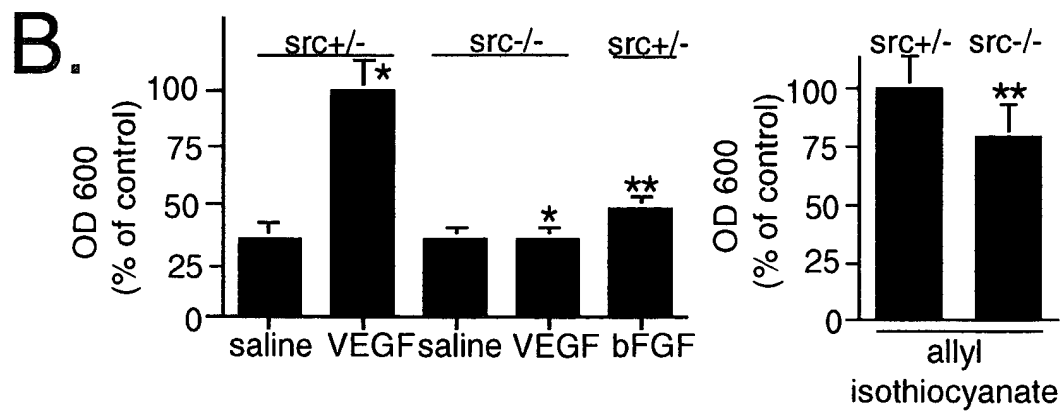
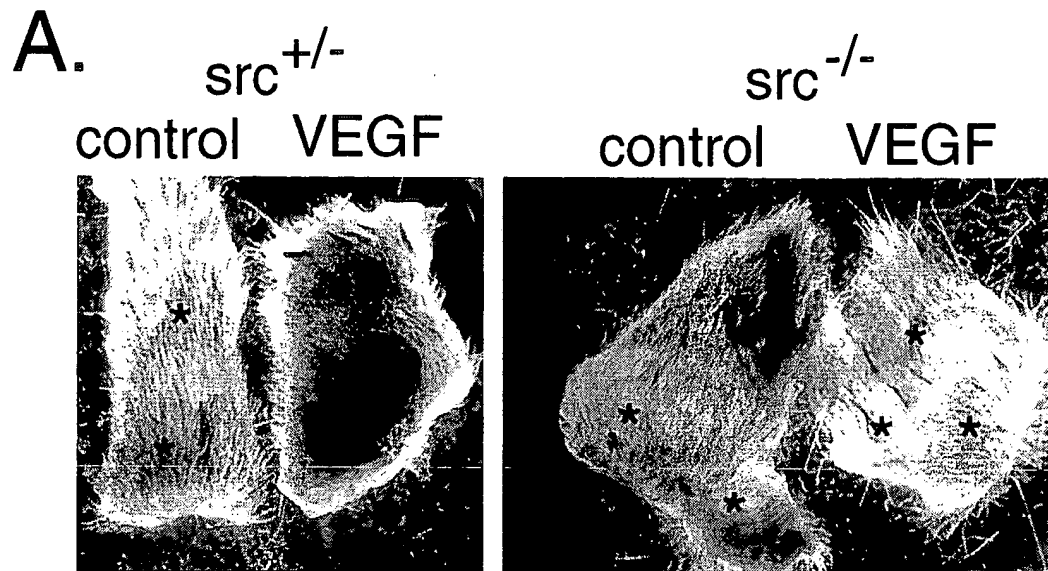
# FIG. 4

(SEQ ID NO: 4)

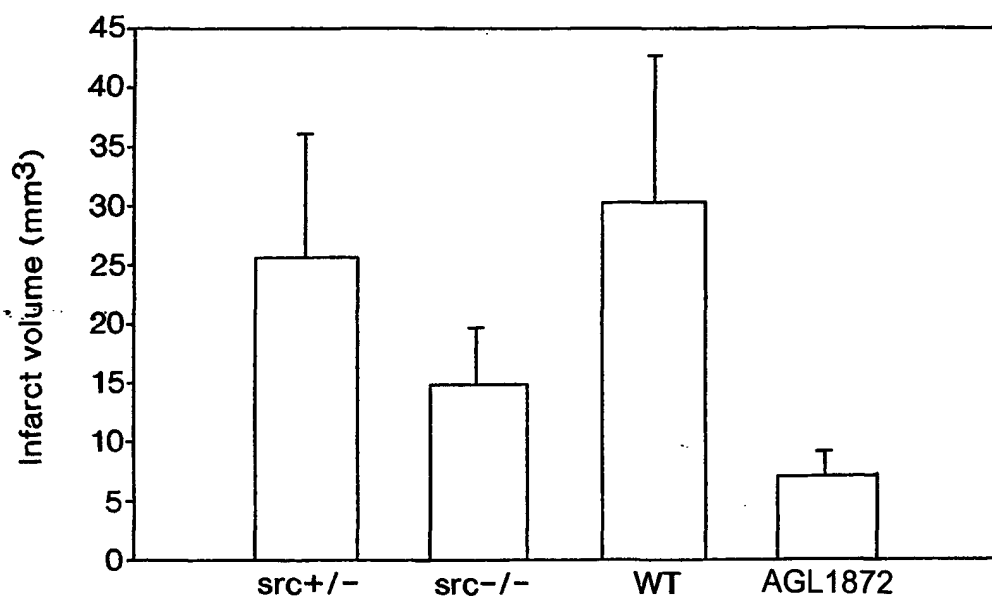
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Arg	Pro	Glu	Asn	Thr	Pro	Glu	Pro	Val	Ser	Thr	Ser	Val	Ser	His	Tyr	20	25	30	
Gly	Ala	Glu	Pro	Thr	Thr	Val	Ser	Pro	Cys	Pro	Ser	Ser	Ser	Ala	Lys	35	40	45	
Gly	Thr	Ala	Val	Asn	Phe	Ser	Ser	Leu	Ser	Met	Thr	Pro	Phe	Gly	Gly	50	55	60	
Ser	Ser	Gly	Val	Thr	Pro	Phe	Gly	Gly	Ala	Ser	Ser	Ser	Phe	Ser	Val	65	70	75	80
Val	Pro	Ser	Ser	Tyr	Pro	Ala	Gly	Leu	Thr	Gly	Gly	Val	Thr	Ile	Phe	85	90	95	
Val	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	Thr	Glu	Asp	Leu	Ser	Phe	100	105	110	
Lys	Lys	Gly	Glu	Arg	Phe	Gln	Ile	Asn	Asn	Thr	Glu	Gly	Asp	Trp		115	120	125	
Trp	Glu	Ala	Arg	Ser	Ile	Ala	Thr	Gly	Lys	Asn	Gly	Tyr	Ile	Pro	Ser	130	135	140	
Asn	Tyr	Val	Ala	Pro	Ala	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp	Tyr	Phe	145	150	155	160
Gly	Lys	Met	Gly	Arg	Lys	Asp	Ala	Glu	Arg	Leu	Leu	Leu	Asn	Pro	Gly	165	170	175	
Asn	Gln	Arg	Gly	Ile	Phe	Leu	Val	Arg	Glu	Ser	Glu	Thr	Thr	Lys	Gly	180	185	190	
Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Glu	Ile	Arg	Gly	Asp	Asn	195	200	205	
Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	210	215	220	
Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Leu	Gln	Lys	Leu	Val	Lys	His	Tyr	225	230	235	240
Thr	Glu	His	Ala	Asp	Gly	Leu	Cys	His	Lys	Leu	Thr	Thr	Val	Cys	Pro	245	250	255	
Thr	Val	Lys	Pro	Gln	Thr	Gln	Gly	Leu	Ala	Lys	Asp	Ala	Trp	Glu	Ile	260	265	270	
Pro	Arg	Glu	Ser	Leu	Arg	Leu	Glu	Val	Lys	Leu	Gly	Gln	Gly	Cys	Phe	275	280	285	
Gly	Glu	Val	Trp	Met	Gly	Thr	Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Ile	290	295	300	
Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Met	Pro	Glu	Ala	Phe	Leu	Gln	Glu	305	310	315	320
Ala	Gln	Ile	Met	Lys	Lys	Leu	Arg	His	Asp	Lys	Leu	Val	Pro	Leu	Tyr	325	330	335	
Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe	Met	Ser	340	345	350	
Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Glu	Gly	Asp	Gly	Lys	Tyr	Leu	355	360	365	
Lys	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Ile	Ala	Asp	Gly	Met	370	375	380	
Ala	Tyr	Ile	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala	385	390	395	400
Asn	Ile	Leu	Val	Gly	Glu	Asn	Leu	Val	Cys	Lys	Ile	Ala	Asp	Phe	Gly	405	410	415	
Leu	Ala	Arg	Leu	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Gln	Gly	Ala	420	425	430	

# FIG. 4 cont.

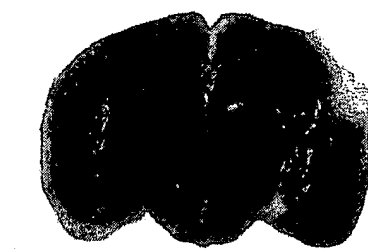
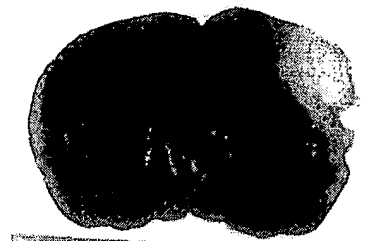
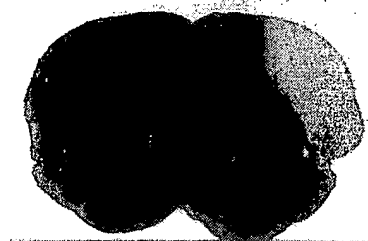
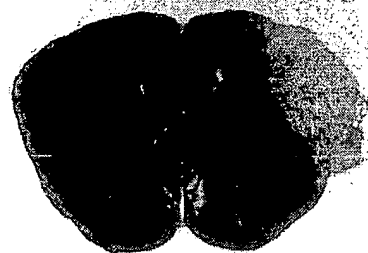
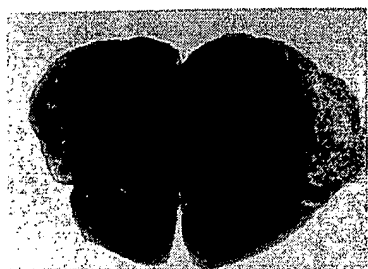
Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Tyr	Gly	Arg
		435					440					445			
Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Gln	Thr	Glu
	450					455					460				
Leu	Val	Thr	Lys	Gly	Arg	Val	Pro	Tyr	Pro	Gly	Met	Val	Asn	Arg	Glu
465					470					475					480
Val	Leu	Glu	Gln	Val	Glu	Arg	Gly	Tyr	Arg	Met	Pro	Cys	Pro	Gln	Gly
			485						490					495	
Cys	Pro	Glu	Ser	Leu	His	Glu	Leu	Met	Asn	Leu	Cys	Trp	Lys	Lys	Asp
			500					505					510		
Pro	Asp	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Ile	Gln	Ser	Phe	Leu	Glu	Asp
	515						520					525			
Tyr	Phe	Thr	Ala	Thr	Glu	Pro	Gln	Tyr	Gln	Pro	Gly	Glu	Asn	Leu	
	530					535					540				



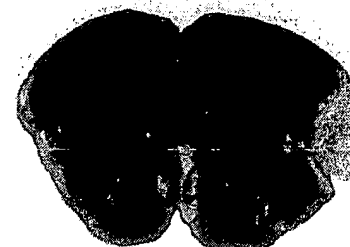
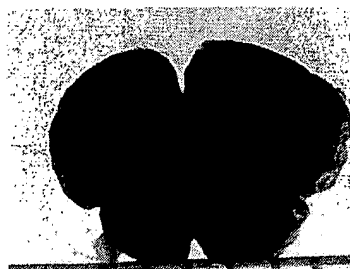
**FIG. 5**



**FIG. 6**

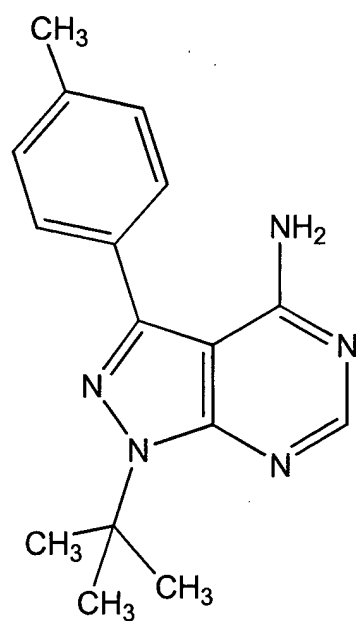


control

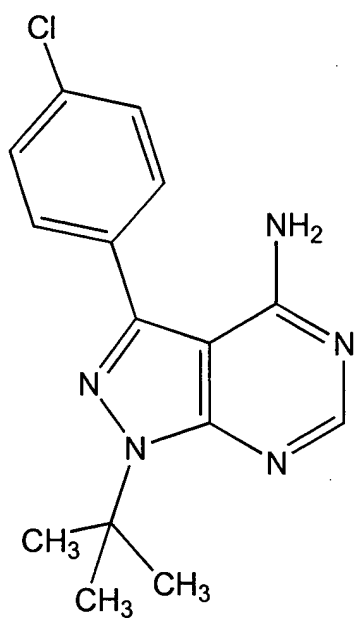


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**FIG. 7**

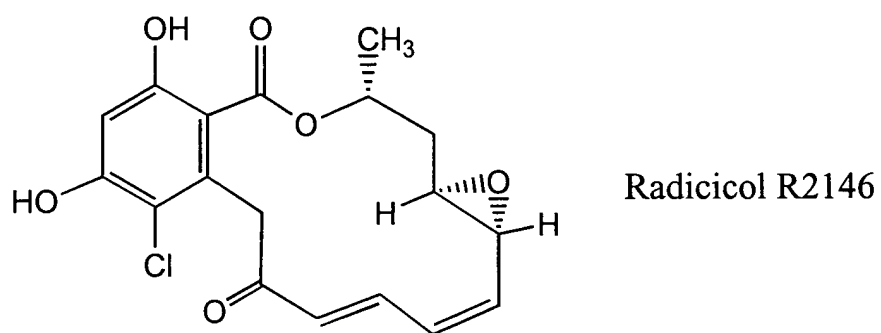
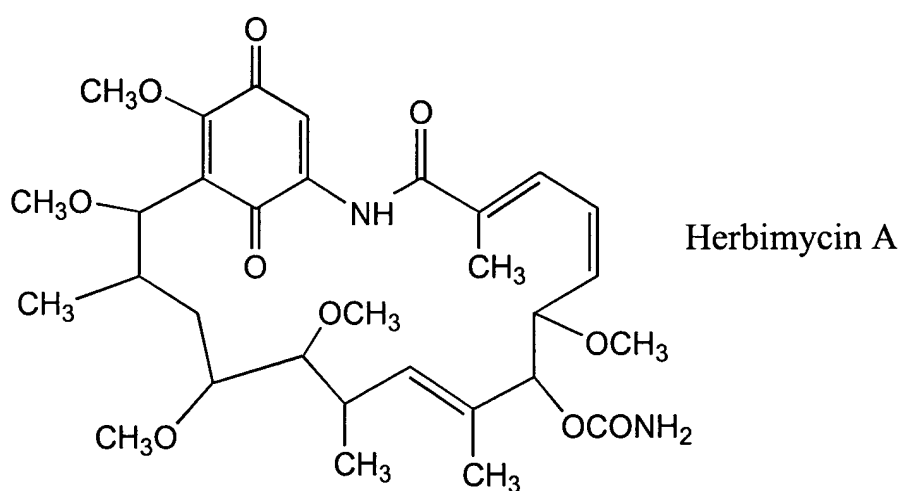
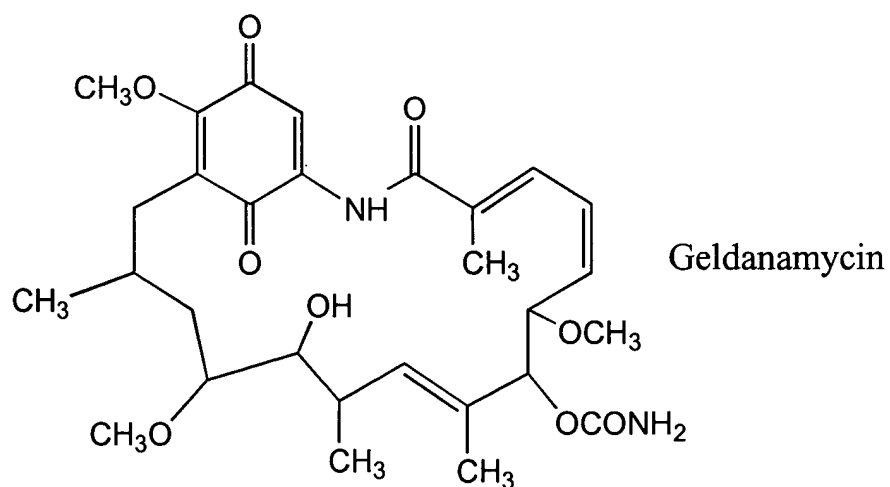


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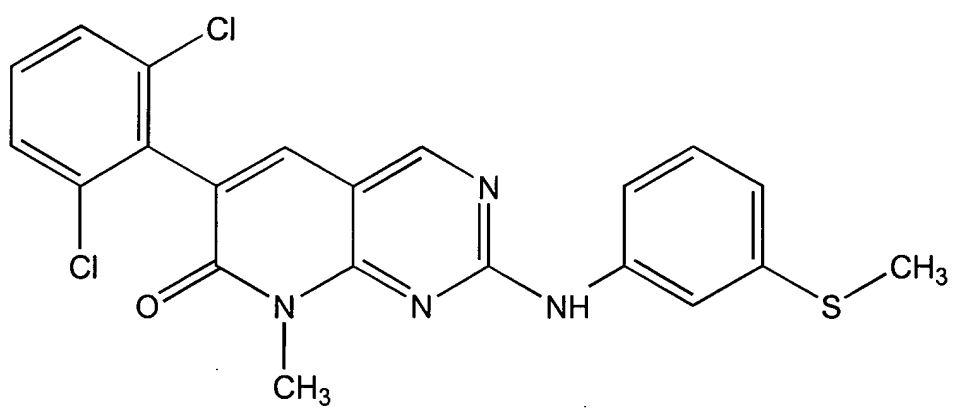


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**FIG. 8**



**FIG. 9**



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**FIG. 10**



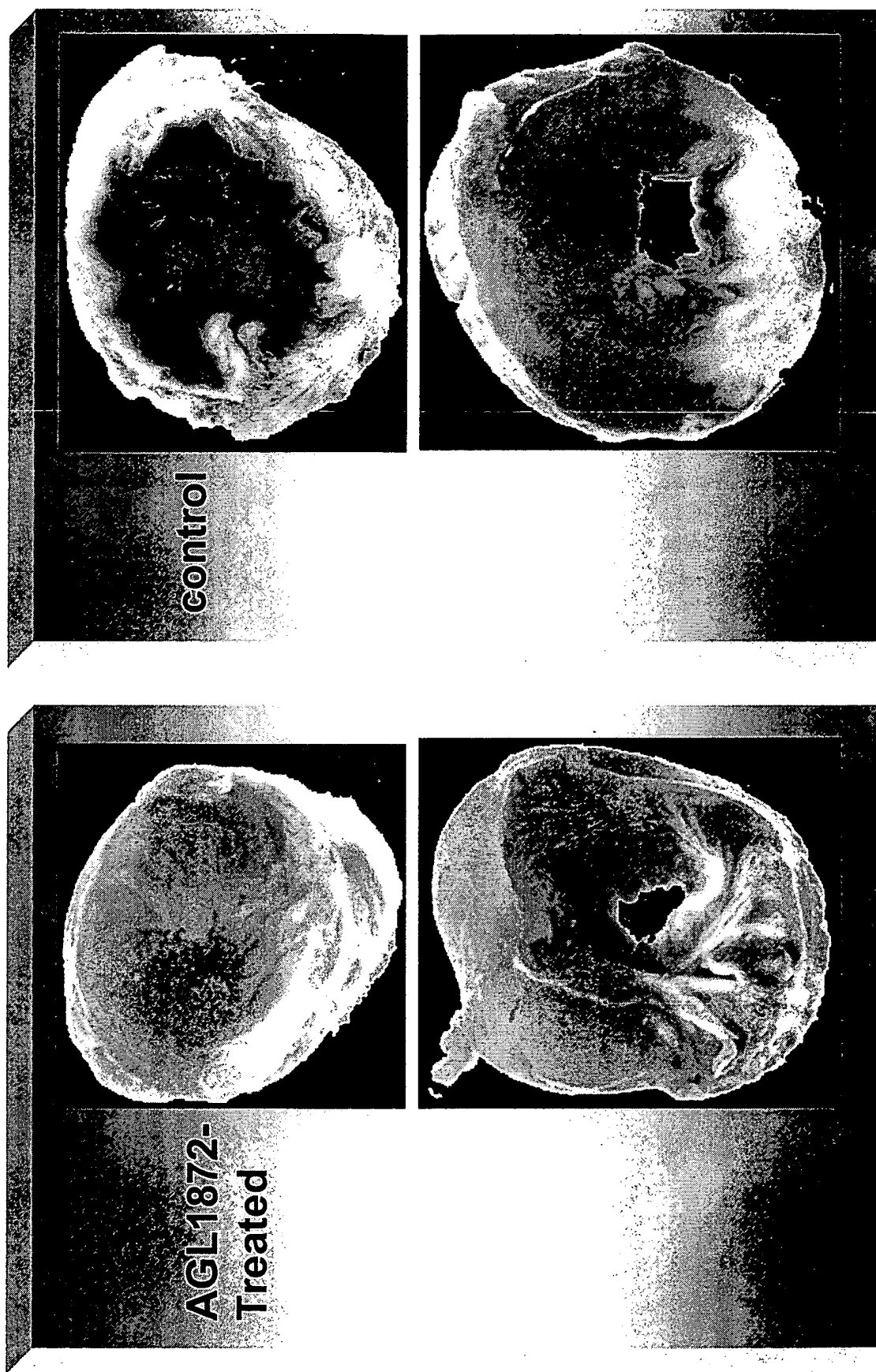


FIG. 11

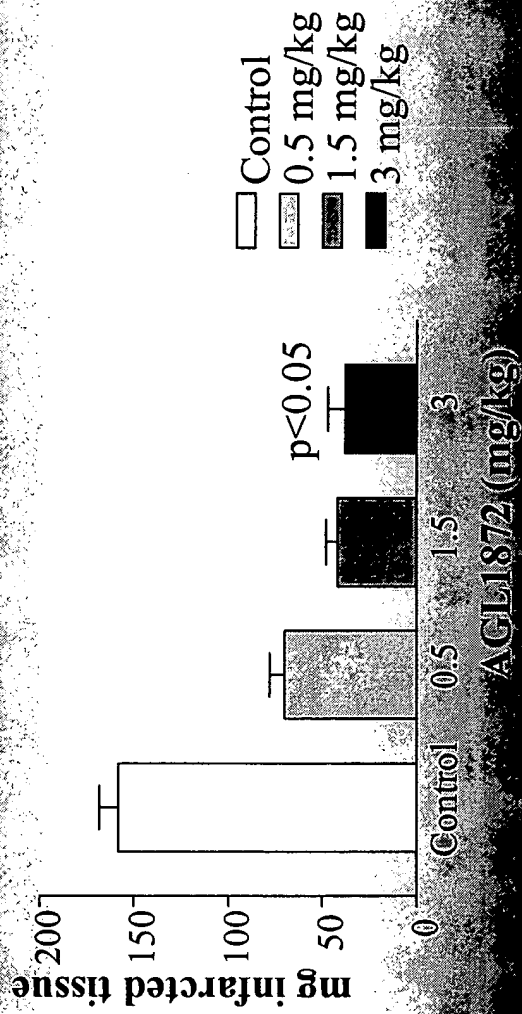


FIG. 12

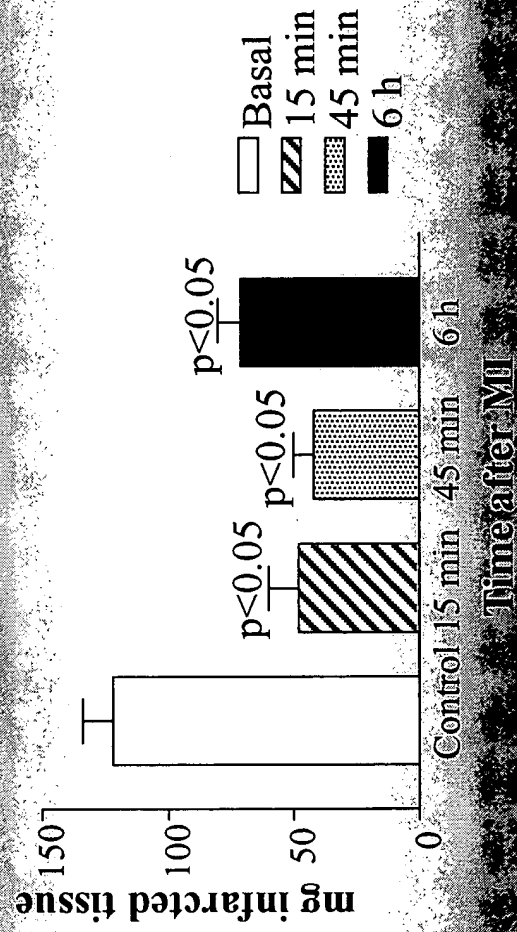


FIG. 13

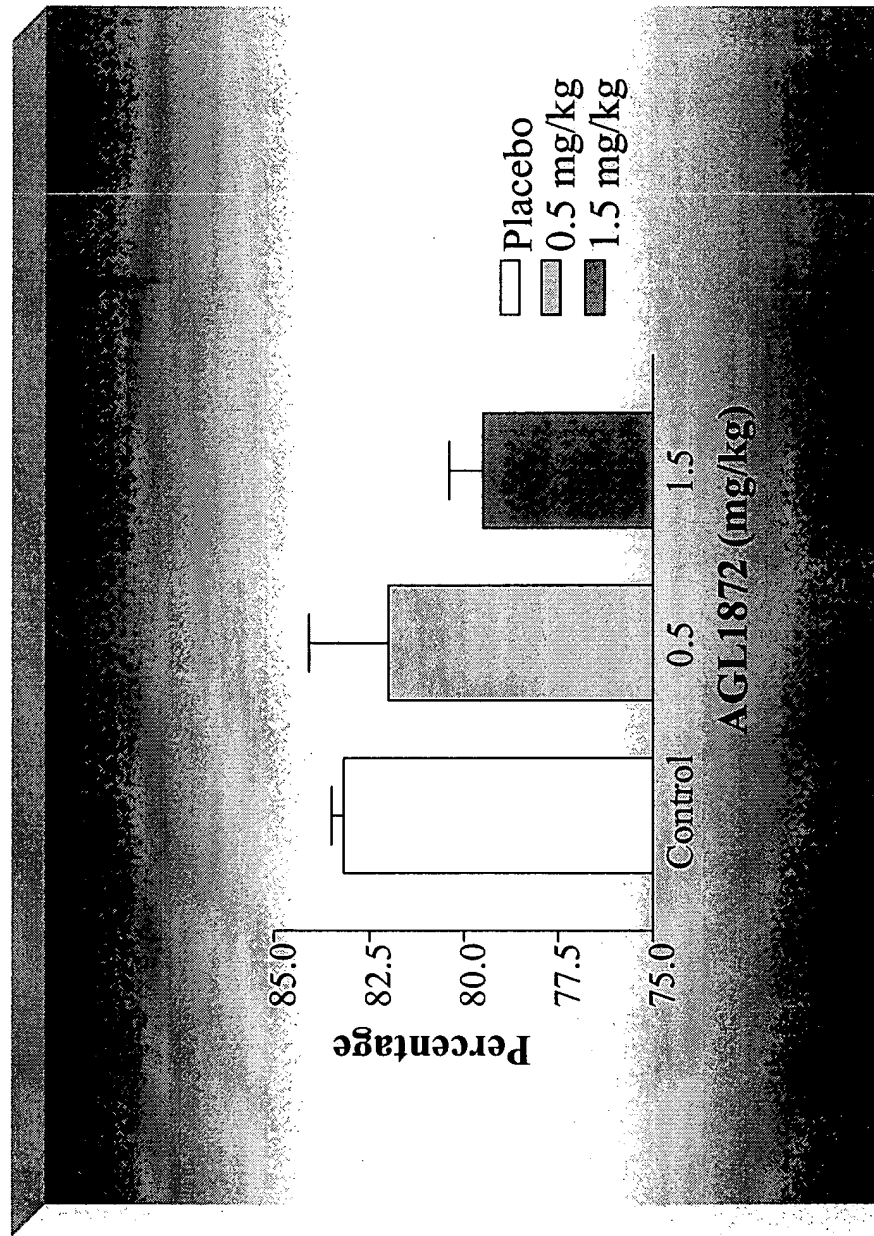


FIG. 14